

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/576,906
Source: IFWO
Date Processed by STIC: 2/20/07

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IFWO

RAW SEQUENCE LISTING

DATE: 02/20/2007

PATENT APPLICATION: US/10/576,906

TIME: 14:53:50

Input Set : A:\19781.seq.txt

Output Set: N:\CRF4\02152007\J576906.raw

3 <110> APPLICANT: BARTHOLOMEUSZ, Angeline; Ingrid
 4 LOCARNINI, Stephen, Alister
 5 AYRES, Anna
 6 YUEN, Lilly, Ka, Wai
 7 SASADEUSZ, Joseph, John
 9 <120> TITLE OF INVENTION: HBV VARIANTS DETECTION AND APPLICATION
 11 <130> FILE REFERENCE: 19781
 13 <140> CURRENT APPLICATION NUMBER: 10/576,906
 14 <141> CURRENT FILING DATE: 2006-04-21
 16 <150> PRIOR APPLICATION NUMBER: AU2003905776
 17 <151> PRIOR FILING DATE: 2003-10-21
 19 <150> PRIOR APPLICATION NUMBER: AU2004900962
 20 <151> PRIOR FILING DATE: 2004-02-25
 22 <160> NUMBER OF SEQ ID NOS: 42
 24 <170> SOFTWARE: PatentIn version 3.2
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 27 <211> LENGTH: 1007
 28 <212> TYPE: DNA
 29 <213> ORGANISM: hepatitis B virus
 31 <400> SEQUENCE: 1
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 36 agacctgctg gtggctccag ttccggaaca gtaaaccctg ttccgactac tgcctctccc 180
 38 atatcgtaaa tcttctcgag gactggggac cctgcgccga atatggagag caccacatca 240
 40 ggattcctag caccctgctc cgtgtttacag gcgggggttt tcttggtgac aagaatcctc 300
 42 acaataccaa agagtctaga ctcggtggtg acttctctca attttctagg gggagcacc 360
 44 acgtgtcctg gccaaaattt gcagtcacca acctccaatc actcaccaac ctcttgctc 420
 46 ccaatttgct ctgggttatcg ctggatgtgt ctgcggcggt ttatcatctt cctcttcac 480
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 52 cctgctcaag gaacctctat gtttccctct tgttgctgta caaaaccttc ggacggaaat 660
 54 tgcacttgta ttcccatccc atcatcttg gctttcgtaa gattcctatg ggagtgggccc 720
 56 tcagtcctgt tctcctggtt cagtttacta gtgccatttg ttcagtgggt cgtagggcct 780
 58 tccccactg tttggctttc agttatatgg atgatgtggt attgggggccc aagtctgtac 840
 60 aacatcttga atccctttat accgctatta ccaattttct tttgtctttg ggtatacatt 900
 62 taaaccctaa taaaaccaag cgttggggct actcccttaa cttcatggga tatgtaattg 960
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 67 <210> SEQ ID NO: 2
 68 <211> LENGTH: 270
 69 <212> TYPE: PRT
 70 <213> ORGANISM: hepatitis B virus
 72 <400> SEQUENCE: 2
 74 Glu Asp Trp Gly Pro Cys Ala Glu Tyr Gly Glu His His Ile Arg Ile

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79          20          25          30
82 Asn Pro His Asn Thr Lys Glu Ser Arg Leu Val Val Asp Phe Ser Gln
83          35          40          45
86 Phe Ser Arg Gly Ser Thr His Val Ser Trp Pro Lys Phe Ala Val Pro
87          50          55          60
90 Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu
91 65          70          75          80
94 Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro Ala
95          85          90          95
98 Ala Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Pro Arg Tyr Val
99          100          105          110
102 Ala Arg Leu Ser Ser Thr Ser Arg Asn Ile Asn Tyr Gln His Gly Thr
103          115          120          125
106 Met Gln Asp Leu His Asp Ser Cys Ser Arg Asn Leu Tyr Val Ser Leu
107          130          135          140
110 Leu Leu Leu Tyr Lys Thr Phe Gly Arg Lys Leu His Leu Tyr Ser His
111 145          150          155          160
114 Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser
115          165          170          175
118 Pro Phe Leu Leu Val Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg
119          180          185          190
122 Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr Met Asp Asp Val Val
123          195          200          205
126 Leu Gly Ala Lys Ser Val Gln His Leu Glu Ser Leu Tyr Thr Ala Ile
127          210          215          220
130 Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro Asn Lys Thr
131 225          230          235          240
134 Lys Arg Trp Gly Tyr Ser Leu Asn Phe Met Gly Tyr Val Ile Gly Ser
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138 Trp Gly Thr Leu Pro Gln Glu His Ile Val Gln Lys Ile Lys
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143 <211> LENGTH: 226
144 <212> TYPE: PRT
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154          20          25          30
157 Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys
158          35          40          45
161 Pro Gly Gln Asn Leu Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
162          50          55          60
165 Cys Pro Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
166 65          70          75          80
169 Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val

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173 Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly
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178          115          120          125
181 Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
182          130          135          140
185 Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Val Arg
186 145          150          155          160
189 Phe Leu Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Phe Ser Leu Leu
190          165          170          175
193 Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
194          180          185          190
197 Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile
198          195          200          205
201 Leu Asn Pro Phe Ile Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
202          210          215          220
205 Tyr Ile
206 225
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210 <211> LENGTH: 982
211 <212> TYPE: DNA
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214 <400> SEQUENCE: 4
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219 ttcaggaaca gtaaaccctg ttccgacttc tgtctctcac acatcgtaa tcttctcgag      180
221 gattgggggtc cctgcgctga acatggagaa catcacatca ggattcctag gacccctgct      240
223 cgtgttacag gcgggggttt tcttggtgac aagaatcctc acaataccgc agagtctaga      300
225 ctcggtgtgg acttctctca attttctagg gggaactacc gtgtgtcttg gccaaaattc      360
227 gcagtcacca acctccaatc actcaccaac ctctgtcctc ccaacttgctc ctggttatcg      420
229 ctggatgtat ctgcggcggt ttatcatctt cctcttcata ctgctgctat gcctcatctt      480
231 cttgttggtt cttctgggac atcaaggtat gttgccggtt tgtcctctaa ttccaggatc      540
233 ttcaaccacc agcacgggac catgcagaac ctgcacgact cctgctcaag gaaactctat      600
235 gtatccctcc tggtgctgta ccaaaccctc ggacggaaat tgcacctgta ttcccatccc      660
237 atcatcctgg gctttcggaa aattcctatg ggagtgggcc tcagcccggt tctcctggct      720
239 cagtttacta gtgccatttg ttcagtgggt cgtagggtt tccccactg tttggctttc      780
241 agttatatgg atgatgtggt attgggggcc aagtctgtat cgcattctga gtcccttttt      840
243 accgctgtta ccaattttct tttgtctttg ggtatacatt taaaccctca caaaacaaaa      900
245 agatgggggtc actctttaca tttcatgggc tatgtcattg gatgttatgg gtcattgcca      960
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253 <213> ORGANISM: hepatitis B virus
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262          20          25          30
265 Asn Pro His Asn Thr Ala Glu Ser Arg Leu Val Val Asp Phe Ser Gln
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269 Phe Ser Arg Gly Asn Tyr Arg Val Ser Trp Pro Lys Phe Ala Val Pro
270          50          55          60
273 Asn Leu Gln Ser Leu Thr Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu
274 65          70          75          80
277 Ser Leu Asp Val Ser Ala Ala Phe Tyr His Leu Pro Leu His Pro Ala
278          85          90          95
281 Ala Met Pro His Leu Leu Val Gly Ser Ser Gly Leu Ser Arg Tyr Val
282          100         105         110
285 Ala Arg Leu Ser Ser Asn Ser Arg Ile Phe Asn His Gln His Gly Thr
286          115         120         125
289 Met Gln Asn Leu His Asp Ser Cys Ser Arg Lys Leu Tyr Val Ser Leu
290          130         135         140
293 Leu Leu Leu Tyr Gln Thr Phe Gly Arg Lys Leu His Leu Tyr Ser His
294 145          150         155         160
297 Pro Ile Ile Leu Gly Phe Arg Lys Ile Pro Met Gly Val Gly Leu Ser
298          165         170         175
301 Pro Phe Leu Leu Ala Gln Phe Thr Ser Ala Ile Cys Ser Val Val Arg
302          180         185         190
305 Arg Ala Phe Pro His Cys Leu Ala Phe Ser Tyr Met Asp Asp Val Val
306          195         200         205
309 Leu Gly Ala Lys Ser Val Ser His Leu Glu Ser Leu Phe Thr Ala Val
310          210         215         220
313 Thr Asn Phe Leu Leu Ser Leu Gly Ile His Leu Asn Pro His Lys Thr
314 225          230         235         240
317 Lys Arg Trp Gly His Ser Leu His Phe Met Gly Tyr Val Ile Gly Cys
318          245         250         255
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322          260         265
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326 <211> LENGTH: 226
327 <212> TYPE: PRT
328 <213> ORGANISM: hepatitis B virus
330 <400> SEQUENCE: 6
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337          20          25          30
340 Asp Ser Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Thr Thr Val Cys
341          35          40          45
344 Leu Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
345          50          55          60
348 Cys Pro Pro Thr Cys Pro Gly Tyr Arg Trp Met Tyr Leu Arg Arg Phe
349 65          70          75          80
352 Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
353          85          90          95
356 Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly

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357          100          105          110
360 Ser Ser Thr Thr Ser Thr Gly Pro Cys Arg Thr Cys Thr Thr Pro Ala
361          115          120          125
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365          130          135          140
368 Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Gly Lys
369 145          150          155          160
372 Phe Leu Trp Glu Trp Ala Ser Ala Arg Phe Ser Trp Leu Ser Leu Leu
373          165          170          175
376 Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
377          180          185          190
380 Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Arg Ile
381          195          200          205
384 Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
385          210          215          220
388 Tyr Ile
389 225
393 <210> SEQ ID NO: 7
394 <211> LENGTH: 1045
395 <212> TYPE: DNA
396 <213> ORGANISM: hepatitis B virus
398 <400> SEQUENCE: 7
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403 aagctctgct agatcccaga gtgagggggc tatattttcc tgctgggtggc tccagttccg      180
405 gaacagtaaa ccctgttccg actactgcct ctcccatatc gtcaatcttc tcgaggactg      240
407 gggaccctgc accgaacatg gagagcacca catcaggatt cctaggaccc ctgctcgcgt      300
409 tacaggcggg gtttttcttg ttgacaagaa tcctcacaat accacagagt ctagactcgt      360
411 ggtggacttc tctcaatttt ctagggggaa cacccaagtg tcctggccaa aatttgcagt      420
413 ccccaacctc caatcactca ccaacctctt gtctctcaat ttgtcctggg tatcgttgga      480
415 tgtgtctgct gcgttttatc atcttctctt ccactcctgt gctatgcctc atcttcttgt      540
417 ggggtcttct ggactaccaa ggtatgttgc cgttttgtcc tctacttcca ggaacatcaa      600
419 ctaccagcac gggaccatgc aagacctgca cgactcctgc tcaaggaacc tctatgtttc      660
421 cctcttggtg ctgtacaaaa ccttcggacg gaaattgcac ttgtattccc atcccatcat      720
423 cttgggcttt cgcaagattc ctatgggagt gggcctcagt ccgtttctcc tggctcagtt      780
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429 tgttaccaat tttcttttgt ctttgggtat acatttaaac cctactaaaa ccaaactgtg      960
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437 <211> LENGTH: 271
438 <212> TYPE: PRT
439 <213> ORGANISM: hepatitis B virus
441 <400> SEQUENCE: 8
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448          20          25          30

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/576,906

DATE: 02/20/2007
TIME: 14:53:51

Input Set : A:\19781.seq.txt
Output Set: N:\CRF4\02152007\J576906.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; Xaa Pos. 208
Seq#:12; Xaa Pos. 172
Seq#:14; Xaa Pos. 288
Seq#:15; Xaa Pos. 298,300
Seq#:27; Xaa Pos. 160
Seq#:30; Xaa Pos. 95
Seq#:32; Xaa Pos. 312
Seq#:33; Xaa Pos. 309,327
Seq#:38; Xaa Pos. 115,147,239
Seq#:39; Xaa Pos. 134,148,240
Seq#:41; Xaa Pos. 247
Seq#:42; Xaa Pos. 142,247

VERIFICATION SUMMARY

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Input Set : A:\19781.seq.txt

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L:572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:192
L:755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:160
L:895 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:272
L:997 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:288
L:1689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:144
L:1844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:80
L:2016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:304
L:2122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:304
M:341 Repeated in SeqNo=33
L:2405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:112
M:341 Repeated in SeqNo=38
L:2508 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:128
M:341 Repeated in SeqNo=39
L:2656 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:240
L:2722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:128
M:341 Repeated in SeqNo=42